



amdt 10

SEQUENCE LISTING

<110> Oklahoma Medical Research Foundation
Sauer, Brian Lee
Rufer, Andreas Walter

<120> Method for Selecting Recombinase Variants with Altered Specificity

<130> OMRF 178

<140> 09/544,045

<141> 2000-04-06

<150> 60/127,977

<151> 1999-04-06

<160> 68

<170> PatentIn version 3.1

<210> 1

<211> 343

<212> PRT

<213> Artificial Sequence

<220>

<223> Cre

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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala

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Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn	85		90		95	
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Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	115		120		125	
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	130		135		140	
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn	145		150		155	160
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu	165		170		175	
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	180		185		190	
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	195		200		205	
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp	210		215		220	
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys	225		230		235	240
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu	245		250		255	
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile						

260

265

270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
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His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
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Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
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 <223> N at positions 1-3 can be A, T, G, or C.

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 <222> (6)..(7)
 <223> N at positions 6 and 7 can be A, T, G, or C.

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<220>
 <223> variant lox sites

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 <223> N at positions 1-3 can be A, G, C, or T

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 <223> N at positions 6 and 7 can be A, T, G, C,

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 <222> (14)..(21)
 <223> N at positions 14-21 can A, G, T, or C

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 <221> misc_feature
 <222> (28)..(29)
 <223> N at postions 28 and 29 can be A, T, G, or C

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 <221> misc_feature
 <222> (32)..(34)
 <223> N at postiions 32-34 can be A, T, G, or C

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<223> variant lox sites

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<223> Specific and non-specific sequences for Cre recombinase

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<222> (32)..(34)

<223> N at positions 32-34 can be A, T, G, or C

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<223> primer

<400> 11

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<223> primer

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<220>
<223> primer

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<220>
<223> primer

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<211> 22
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 20
gtacgtgaga tatctttaac cc
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<210> 21
<211> 22
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<213> artificial sequence

<220>

<223> primer

<400> 21

ttgctggata gtttttactg cc

22

<210> 22

<211> 45

<212> DNA

<213> artificial sequence

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<223> primer

<400> 22

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<210> 23

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<223> primer

<400> 23

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<223> primer

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<222> (17)..(25)
<223> N at positions 17-25 can be A, T, G, or C

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<210> 27
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<222> (17)..(25)
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120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcggcattg tgcaagtga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
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cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccagggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
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atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgcca ggatcagggt
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gctggttagc accgcagggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt

780

cagaaaaaat ggtgttgccg cgcacatctgc caccagccag ctatcaactc gcgccttgga
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agggatTTTT gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

atacctggcc tggctctggac acagtgcgcc tgtcggagcc gcgcgagata tggcccgcgc
960

tggagtTTTca ataccggaga tcatgcaagc tggtggtctgg accaatgtaa atattgtcat
1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
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tcagcctgat acagattaaa tcagaacgca ga
1172

<210> 29

<211> 1172

<212> DNA

<213> artificial sequence

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<223> mxoxox1

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atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
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tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttctactg gttatgcggc ggatccgaaa
420

agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccagggtt cgttctactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
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atttctgggg attgcttata acaccctgtt acgtatagcc gaaattgccg ggatcagggt
600

taaagatatc tcacgtacta acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctggttagc accgcagggtg tagagaaggc acttagtctg ggggtaacta aactggtcga
720

gcgatggatt tccatctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg
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agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
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atacctggcc tggctctggac acagtgcccg tgtcggagcc gcgcgagata tggcccgcgc
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tggagtttca ataccggaga tcatgcaagc tgggtggctgg accaatgtaa atattgtcat
1020

gaactatatc cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

tcagcctgat acagattaata tcagaacgca ga
1172

<210> 30

<211> 1172

<212> DNA

<213> artificial sequence

<220>

<223> mxoxox2

<400> 30

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caatttactg accgtacacc aaaatttgcc tgcattacct gtcgatgcaa cgagtgatga
120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcataacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcgccatgg tgcaagttga ataaccggaa
240

atgggttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
300

tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcggtc
360

cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
420

agaaaacggt gatgccggtg aacgtgcaaa acaggctcta gcgttcggac gcactgattt
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cgaccagggt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
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atttctgggg attgcttata acaccctggt acgtatagcc gaaattgcca ggatcagggg
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taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
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gctgggttagc accgcagggt tagagaaggc acttagcctg ggggtaacta aactggtcga
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gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
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840

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atacctggcc tggtcggac acagtggccg tgtcggagcc gcgcgagata tggcccgcgc
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tggagtttca ataccggaga tcctgcaagc tggcggctgg tccaatgtaa atattgtcat
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1080

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cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa

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agaaaacgtt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
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960

tggagtttca ataccggaga tcatgcaagc tgggtggctgg accaatgtaa atattgtcat
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gaactatatc cgtaacctgg atagtgaac aggggcaatg gtgcgcctgc tggaagatgg
1080

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120

ggttcgcaag aacctgatgg ccatgttcag ggatcgccag gcgttttctg agcatacctg
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gaaaatgctt ctgtccgttt gccggtcgtg ggcggcatgg tgcaagttga ataaccggaa
240

atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
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tctggcagta aaaactatcc agcaacattt gggccagcta aacatgcttc atcgtcagtc
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cgggctgcca cgaccaagtg acagcaatgc tgtttcactg gttatgcggc ggatccgaaa
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agaaaacggt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
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cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccctggg
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120

ggttcgcaag aacctgatgg acatgttcag ggatcgccag gcgttttctg agcatacctg
180

gaaaatgctt ctgtccgttt gccggtcgtg ggcgccatgg tgcaagttga ataaccggaa
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atggtttccc gcagaacctg aagatgttcg cgattatctt ctatatcttc aggcgcgcgg
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420

agaaaacggt gatgccggtg aacgtgcaaa acaggctcta gcgttcgaac gcactgattt
480

cgaccaggtt cgttcactca tggaaaatag cgatcgctgc caggatatac gtaatctggc
540

atttctgggg attgcttata acaccctggt acgtatagcc gaaattgcca ggatcagggg
600

taaagatatc tcacgtactg acggtgggag aatgttaatc catattggca gaacgaaaac
660

gctgggttagc accgcaggtg tagagaaggc acttagcctg ggggtaacta aactggtcga
720

gcgatggatt tccgtctctg gtgtagctga tgatccgaat aactacctgt tttgccgggt
780

cagaaaaaat ggtgttgccg cgccatctgc caccagccag ctatcaactc gcgccttggg
840

agggattttt gaagcaactc atcgattgat ttacggcgct aaggatgact ctggtcagag
900

ataccaggcc tgggtctggac acagtgcccg tgcggagacc gcgcgagata tggcccgcgc
960

tggagtttca ataccggaga tcatgcaagc tgggtggctgg tccaatgtaa atattgtcat

1020

gaactatatac cgtaacctgg atagtgaaac aggggcaatg gtgcgcctgc tggaagatgg
1080

cgattagcca ttaacgcgta aatgataagc ttggctgttt tggcggatga gagaagattt
1140

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1172

<210> 35
<211> 343
<212> PRT
<213> artificial sequence

<220>
<223> mxoxox1

<400> 35

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

Ile Ser Ile Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 36
 <211> 343
 <212> PRT
 <213> artificial sequence

<220>
 <223> mxoxox2

<400> 36

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Gly Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Gly Gln Leu
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 37
 <211> 343
 <212> PRT
 <213> artificial sequence

<220>
 <223> mxoxox3

<400> 37

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Ile
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asn Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Ser Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Gln Trp
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Arg Leu
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Leu Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 38
 <211> 343
 <212> PRT
 <213> artificial sequence

<220>
 <223> mxoxox4

<400> 38

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Cys Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Lys Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 39
 <211> 343
 <212> PRT
 <213> artificial sequence

<220>
 <223> mxoxox5

<400> 39

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Ala Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Gln Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Gln Val Glu Arg Trp
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 40
 <211> 343
 <212> PRT
 <213> artificial sequence

<220>
 <223> mxoxox6

<400> 40

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

Ser Thr Arg Ala Leu Gly Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Gln Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Ser Asn Val Asn Ile
 305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335

Arg Leu Leu Glu Asp Gly Asp
 340

<210> 41

<211> 13

<212> DNA

<213> artificial sequence

<220>

<223> loxP

<220>

<221> misc_feature

<222> (6)..(7)

<223> nn is either TT, TG, GT, GG, TC, CC, or AA

<400> 41

ataacnncgt ata

13

<210> 42

<211> 13

<212> DNA

<213> artificial sequence

<220>

<223> loxK2

<400> 42

ataacaacgt ata
13

<210> 43

<211> 13

<212> DNA

<213> artificial sequence

<220>

<223> loxK1

<400> 43

atacctttgt ata
13

<210> 44

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> loxP

<400> 44

ataacttcgt atataccttt ctatagcaag ttat
34

<210> 45

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> loxK2

<400> 45

ataacaacgt atataccttt ctatagcttg ttat
34

<210> 46

<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK1

<400> 46
atacctttgt atataccttt ctatagaaag gtat
34

<210> 47
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GG'

<400> 47
ataacggcgt atataccttt ctatagcccg ttat
34

<210> 48
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'CC'

<400> 48
ataaccccggt atataccttt ctatagcggg ttat
34

<210> 49
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TC'

<400> 49
ataactccgt atataccttt ctatagcgag ttat

34

<210> 50
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'GT'

<400> 50
ataacgtcgt atataccttt ctatagcacg ttat
34

<210> 51
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2 'TG'

<400> 51
ataactgcgt atataccttt ctatagccag ttat
34

<210> 52
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> LoxP

<400> 52
ataacttcgt ataattgtatg ctatacgaag ttat
34

<210> 53
<211> 34
<212> DNA
<213> artificial sequence

<220>

<223> LoxK1

<400> 53
gagcctttgt atataccttt ctatacaaag gctt
34

<210> 54
<211> 34
<212> DNA
<213> artificial sequence

<220>
<223> loxK2

<400> 54
gatacaacgt atataccttt ctatacggtg tatt
34

<210> 55
<211> 64
<212> DNA
<213> artificial sequence

<220>
<223> Gene

<400> 55
gctagcgaat tcgagcttcg gtacccgggg atcctctaga gtcgacctgc aggcatgcaa
60

gctt
64

<210> 56
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 56
agcttgagg ctatcatgtc gaccaagcta gca
33

<210> 57
<211> 33
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 57
gatctgctag cttggctcgac atgatagcct cca
33

<210> 58
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 58
gatctgatat ctgcggccgc tgacgtgact cgagt
35

<210> 59
<211> 35
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 59
ctagactcga gtcacgtcag cggccgcaga tatca
35

<210> 60
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 60
gaagttccta ttc
13

<210> 61
<211> 8
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 61
tctagaaa
8

<210> 62
<211> 13
<212> DNA
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<220>
<223> oligonucleotide

<400> 62
gtataggaac ttc
13

<210> 63
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 63
gaagttccta ttccgaagtt cctattc
27

<210> 64
<211> 6
<212> DNA
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<220>
<223> oligonucleotide

<400> 64
tctaga
6

<210> 65
<211> 13
<212> DNA
<213> artificial sequence

Handwritten: 212
<220>
<223> oligonucleotide

<400> 65
gaagttcata ttc
13

<210> 66
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 66
gtatatgaac ttc
13

<210> 67
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 67
gaagttacta ttc
13

<210> 68
<211> 13
<212> DNA
<213> artificial sequence

<220>
<223> oligonucleotide

<400> 68
gtatagtaac ttc
13

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conce